

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: October 23, 2002, 20:18:52 ; Search time 1839 Seconds
(without alignments)
3971.376 Million cell updates/sec

Title: US-09-728-446-819
Perfect score: 349
Sequence: 1 tattatatgttaagtaactctg.....gnnttgcccttgaaggttg 349

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sls:*
28: em_un:*
29: em_vl:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htgo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
------------	-------	-------------	--------	-------	-------------

1	151.4	43.4	1328	10	BC004743	BC004743 Mus muscu
2	151.4	43.4	1345	10	MMU30839	U30839 Mus musculu
3	146.6	42.0	1292	10	MMU89990	U89990 Mus musculu
4	146.6	42.0	164796	2	AC083947	AC083947 Mus muscu
5	135.4	38.8	881	10	AF268469	AF268469 Rattus no
6	135.4	38.8	1380	10	AB039664	AB039664 Rattus no
7	133.2	38.2	879	4	AF268466	AF268466 Bos tauru
8	132.2	37.9	825	10	AF048829	AF048829 Rattus no
9	132.2	37.9	828	10	AF048830	AF048830 Rattus no
10	130.6	37.4	1077	9	HSU90943	U90943 Homo sapien
11	130.6	37.4	1209	6	AR017815	AR017815 Sequence
12	130.6	37.4	1364	9	AK058201	AK058201 Homo sapi
13	130.6	37.4	1393	6	AR103434	AR103434 Sequence
14	130.6	37.4	1851	9	BC002456	BC002456 Homo sapi
15	127.4	36.5	879	4	AF209727	AF209727 Oryctolag
16	122	35.0	879	4	AF268463	AF268463 Sus scrof
17	121	34.7	163272	9	CNS01DUT	AL133368 Human chr
18	82.2	23.6	237	4	BTA299423	AJ299423 Bos tauru
19	69.8	20.0	1317	10	BC003731	BC003731 Mus muscu
20	69.8	20.0	1662	10	MMU30838	U30838 Mus musculu
21	67.4	19.3	324	6	AX341725	AX341725 Sequence
22	67.4	19.3	848	9	HS3VDAC3	AF151681 Homo sapi
23	67.4	19.3	89921	2	AF170802	AF170802 Homo sapi
24	67.4	19.3	94060	2	AF216673	AF216673 Homo sapi
25	67.4	19.3	164419	2	AC104387	AC104387 Homo sapi
26	67.4	19.3	165041	2	AC107885	AC107885 Homo sapi
27	66.6	19.1	930	10	AF268468	AF268468 Rattus no
28	66.6	19.1	1715	10	AB039663	AB039663 Rattus no
29	65	18.6	885	4	BTA288914	AJ288914 Bos tauru
30	65	18.6	907	4	AF268462	AF268462 Sus scrof
31	63.4	18.2	920	4	AF268465	AF268465 Bos tauru
32	63.4	18.2	1404	9	HUMVDAC2X	L06328 Human volta
33	63.4	18.2	1464	9	HUMPORIN	L08666 Homo sapien
34	63.4	18.2	1477	9	BC012883	BC012883 Homo sapi
35	63.4	18.2	1522	9	BC000165	BC000165 Homo sapi
36	59.6	17.1	130049	2	AC073296	AC073296 Mus muscu
37	59.6	17.1	154256	2	AC073295	AC073295 Mus muscu
38	59.6	17.1	238039	2	AL596103	AL596103 Mus muscu
39	57.4	16.4	647	10	AF441736	AF441736 Mus muscu
40	57.4	16.4	191750	2	AC024113	AC024113 Mus muscu
41	57	16.3	921	4	AF209726	AF209726 Oryctolag
42	56.6	16.2	932	5	AF268470	AF268470 Gallus ga
43	54.8	15.7	94459	10	MMTSDNA	X99946 M.musculus
44	54.8	15.7	230384	2	AL669964	AL669964 Mus muscu
45	54.8	15.7	241432	10	AL589661	AL589661 Mouse DNA

ALIGNMENTS

RESULT 1
BC004743
LOCUS
DEFINITION Mus musculus, voltage-dependent anion channel 3, clone MGC:5955
IMAGE:3583800, mRNA, complete cds.
ACCESSION BC004743
VERSION BC004743.1 GI:13435770
KEYWORDS MGC.
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE
1 (bases 1 to 1328)
AUTHORS Strausberg,R.
TITLE Direct Submission
JOURNAL Submitted (21-MAR-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK
COMMENT NIH-MGC Project URL: http://mgc.ncl.nih.gov
Contact: MGC help desk
Email: cgabs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.

CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
Contact: villalobcm.tmc.edu
Villalon, D.K., Luna, R.A., Hale, S.M., Hulyk, S., Lu, X., Garcia,
A.M., Holloway, M., Telford, B., Hodgson, A., Bouck, J., Yu, W.,
Muzny, D.M., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>
Series: IRAK Plate: 10 Row: 0 Column: 3
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 1463027.
Location/Qualifiers

FEATURES

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/db_xref="taxon:10090"
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model. 10 month old virgin mouse. Taken by biopsy."
/clone_1lb="NCI_CGAP_Mam1"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"
31.882
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KSKLSQNNFALGYKAADFOLHTHVNDGTEFGGSYOKVNERIETISINLAWTAGSNNT
FGIAAKYKIDCRTSLSAKVNNASLIGLYTQTLRPVKLTLSALIDGKNFNAGHKVG
LGFELEA"

CDS
BASE COUNT 393 a 264 c 307 g 364 t
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Best Local Similarity 77.6%; Pred. No. 2.9e-36;
Matches 204; Conservative 0; Mismatches 55; Indels 4; Gaps 3;

OY 88 ATGGCTGCNACTATGGGCTCACCCTTACCCANANGAGTACNGACGCTACTTGGG 147
DB 217 AAGTCTGCAACTATGGGCTCACCCTTACCCAAAAGTGAATACAGACAATCTTGGG 276
OY 148 ACAGACCTTTTNGAGAAATNTGCATGGCTGANGGTTNAACTGACTCTGCATACCAT 207
DB 277 ACAGAAATCTCTGGGAGAAATAG-TTGGCTGAAGGCTTGAAGTCTTGTATACCAT 335
OY 208 ATTNTACCATNCTCCNATCCTTTAGTGCATTTTCCCGGCTCCTATTCGCCNGAT 267
DB 336 ATTTGTACCAACACAGGAA--AGAAGAGTGGGAAATTAAGGCTCTATAGACGGGAT 393
OY 268 TGTNNANTCTCGGACGTAATGTGATNTNNAATTTTCTGACCGACCATCTATGGCT-G 326
DB 394 TGTTTAGTCTCGGACGTAATGTGATATAGATTTTCTGACCGACCATCTATGGCTGG 453
OY 327 TCTGNNTTGGCCTTTGAAGGTTG 349
DB 454 GCTGTGTGGCCTTTGAAGGTTG 476

RESULT 2
LOCUS MMU30839 1345 bp mRNA linear ROD 20-FEB-1997
DEFINITION Mus musculus voltage dependent anion channel 3 mRNA, nuclear gene
ACCESSION U30839
VERSION U30839.1 GI:1463027

KEYWORDS

house mouse.
Mus musculus

SOURCE

house mouse.
Mus musculus

ORGANISM

house mouse.
Mus musculus

REFERENCE

AUTHORS
TITLE
JOURNAL
MEDLINE
REFERENCE
AUTHORS
TITLE
JOURNAL
2 (bases 1 to 1345)
Sampson, M.J., Lovell, R.S., Davison, D. and Craigen, W.J.
Submitted (03-JUL-1995) William Craigen, Molecular and Human
Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX
77030, USA
On Jul 25, 1996 this sequence version replaced gi:1098620.
Location/Qualifiers
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/db_xref="taxon:10090"
/chromosome="8"
/tissue_type="brain"
78.929
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/protein_id="AAB47776.1"
/db_xref="GI:1463028"
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KSKLSQNNFALGYKAADFOLHTHVNDGTEFGGSYOKVNERIETISINLAWTAGSNNT
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LGFELEA"

COMMENT
FEATURES
source
On Jul 25, 1996 this sequence version replaced gi:1098620.
Location/Qualifiers
1.1345
/organism="Mus musculus"
/db_xref="taxon:10090"
/chromosome="8"
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78.929
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KSKLSQNNFALGYKAADFOLHTHVNDGTEFGGSYOKVNERIETISINLAWTAGSNNT
FGIAAKYKIDCRTSLSAKVNNASLIGLYTQTLRPVKLTLSALIDGKNFNAGHKVG
LGFELEA"

CDS
BASE COUNT 373 a 275 c 323 g 374 t
ORIGIN
Query Match 43.4%; Score 151.4; DB 10; Length 1345;
Best Local Similarity 77.6%; Pred. No. 2.9e-36;
Matches 204; Conservative 0; Mismatches 55; Indels 4; Gaps 3;

OY 88 ATGGCTGCNACTATGGGCTCACCCTTACCCANANGAGTACNGACGCTACTTGGG 147
DB 264 AAGTCTGCAACTATGGGCTCACCCTTACCCAAAAGTGAATACAGACAATCTTGGG 323
OY 148 ACAGACCTTTTNGAGAAATNTGCATGGCTGANGGTTNAACTGACTCTGCATACCAT 207
DB 324 ACAGAAATCTCTGGGAGAAATAG-TTGGCTGAAGGCTTGAAGTCTTGTATACCAT 382
OY 208 ATTNTACCATNCTCCNATCCTTTAGTGCATTTTCCCGGCTCCTATTCGCCNGAT 267
DB 383 ATTTGTACCAACACAGGAA--AGAAGAGTGGGAAATTAAGGCTCCTATAGACGGGAT 440
OY 268 TGTNNANTCTCGGACGTAATGTGATNTNNAATTTTCTGACCGACCATCTATGGCT-G 326
DB 441 TGTTTAGTCTCGGACGTAATGTGATATAGATTTTCTGACCGACCATCTATGGCTGG 500
OY 327 TCTGNNTTGGCCTTTGAAGGTTG 349
DB 501 GCTGTGTGGCCTTTGAAGGTTG 523

RESULT 3
LOCUS MMU89990 1292 bp DNA linear ROD 04-OCT-2000
DEFINITION Mus musculus voltage dependent anion channel 3 processed
pseudogene, complete sequence.
ACCESSION U89990
VERSION U89990.1 GI:2290386
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 1292)
AUTHORS Sampson,M.J., Lovell,R.S. and Craigen,W.J.
TITLE The murine voltage-dependent anion channel gene family. Conserved structure and function
JOURNAL J. Biol. Chem. 272 (30), 18966-18973 (1997)
MEDLINE 97373603
PUBMED 9228078
REFERENCE 2 (bases 1 to 1292)
AUTHORS Sampson,M.J., Lovell,R.S. and Craigen,W.J.
TITLE Direct Submission
JOURNAL Submitted (19-FEB-1997) of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
FEATURES
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1. .1292
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/db_xref="taxon:10090"
31. .879
/note="processed pseudogene; similar to voltage dependent anion channel 3"
/codon_start=1
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ORIGIN
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Best Local Similarity 76.4%; Pred. No. 9,1e-35;
Matches 201; Conservative 0; Mismatches 58; Indels 4; Gaps 3;
QY 88 ATGGGCTGCNACTATGGCTCACCTTCACCCANANGAGAGTACNGACGGTACTCTGGG 147
DB 217 AAGGTCTGCACTATGGGCTCACCTTCACCCAAAGTGGAATACAGACACACTCTGGG 276
QY 148 ACAGACCTTTTNGAGAAATGTCATGGCTGANGGTTNAACTGACTCTGCATACCAT 207
DB 277 ACAGAAATCTCTGGGAGATAAG-TTGGCTGAAGGCTTGAACACTGACTCTGCATACCAT 335
QY 208 ATTNTACCATNCNCTCCNATCTTTAGTGCCATTTCCCGGCTCTATGCGCNGNAT 267
DB 336 ATTTGTACCAACACAGGAA--AGAGAGTGGGAATTAAAGGCGCTCTATAGACGGGAT 393
QY 268 TGNNTNANTCTCGGACGTAATGTGATNTNATTTTCGAGCCGACCATCTATGGCT-G 326
DB 394 TGTTTAGTCTCGGACGTAATGTGATATAGATTTCGAAACCGACCATCTATGGCTGG 453
QY 327 TCTGNNTTGGCCTTTGAAGGTG 349
DB 454 GCTGTGTGGCCTTTGAAGGTG 476
RESULT 4
AC083947
LOCUS AC083947 164796 bp DNA linear HTG 07-OCT-2000
DEFINITION Mus musculus chromosome 13 clone RP23-25H6 strain C57BL6/J, WORKING DRAFT SEQUENCE, 12 unordered pieces.
AC083947
AC083947.1 GI:10716596
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 164796)
REFERENCE Beckstrom-Sternberg,S.M., Benjamin,B., Blakesley,R.W., Bouffard,G.G., Dietrich,N.L., Gupta,J., Ho,S.-L., Idol,J., Lee-Lin,S.-Q., Legaspi,R., Lim,M., Maduro,Q.L., Maduro,V.B., Mastriano,S.D., McCloskey,J.C., McDowell,J., Pearson,R., Snyder,B., Stantrilop,S., Thomas,J.W., Thomas,P.J., Tjongson,E.E., Touchman,J.W., Tran,J.T., Vogt,J.L., Walker,M.A., Wetherby,K.D. and Green,E.D.
TITLE NISC Mouse Sequencing Initiative
JOURNAL Unpublished

REFERENCE 2 (bases 1 to 164796)
AUTHORS Green,E.D.
TITLE Direct Submission
JOURNAL Submitted (07-OCT-2000) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA
COMMENT
----- Genome Center
Center: NIH Intramural Sequencing Center
Center code: NISC
Web site: <http://www.nisc.nih.gov>
Contact: nisc_mouse@nih.gov
----- Project Information
Center project name: tw
Center clone name: 025H06
----- Summary Statistics
Sequencing vector: plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 159902 bases at least Q40
Consensus quality: 161129 bases at least Q30
Consensus quality: 161677 bases at least Q20
Insert size: 21400; agarose-fp
Insert size: 163696; sum-of-ctigs
Quality coverage: 4.41x in Q20 bases; agarose-fp
Quality coverage: 5.76x in Q20 bases; sum-of-ctigs

* NOTE: This is a 'working draft' sequence. It currently consists of 12 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
1 3970: contig of 3970 bp in length
* 3971 4070: gap of unknown length
* 4071 10761: contig of 6691 bp in length
* 10762 10861: gap of unknown length
* 10862 17452: contig of 6591 bp in length
* 17453 17552: gap of unknown length
* 17553 26656: contig of 9104 bp in length
* 26657 26756: gap of unknown length
* 26757 36514: contig of 9758 bp in length
* 36515 36614: gap of unknown length
* 36615 49813: contig of 13199 bp in length
* 49814 49913: gap of unknown length
* 49914 60113: contig of 10200 bp in length
* 60114 60213: gap of unknown length
* 60214 73386: contig of 13173 bp in length
* 73387 73486: gap of unknown length
* 73487 91199: contig of 17713 bp in length
* 91200 91299: gap of unknown length
* 91300 115064: contig of 23765 bp in length
* 115065 115164: gap of unknown length
* 115165 139733: contig of 24569 bp in length
* 139734 139833: gap of unknown length
* 139834 164796: contig of 24963 bp in length.
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/strain="C57BL6/J"
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/clone="RP23-25H6"
/clone_lib="RPCI mouse BAC library 23"
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4071. .10761
/note="assembly_fragment"
10862. .17452
/note="assembly_fragment"
17553. .26656
/note="assembly_fragment"
26757. .36514
misc_feature
misc_feature
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47364	a
34055	c
33312	g
48928	t
1137	others

BASE COUNT	259 a	167 c	225 g	230 t
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Tel:81-886-33-7278, Fax:81-886-33-9512)

FEATURES

source

Location/Qualifiers
1..1380

/organism="Rattus norvegicus"

/db_xref="taxon:10116"

90..941

/gene="VDAC3"

90..941

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/protein_id="BAB13475.1"

/db_xref="GI:10119782"

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KSKLCNNFALGYKAEQDLHTHVNDGTEFGSITQVNEK IETSINLAWTAGSNNT
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LGFELEA"

BASE COUNT 402 a 272 c 334 g 372 t
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Query Match 38.8%; Score 135.4; DB 10; Length 1380;
Best Local Similarity 73.8%; Pred. No. 2.8e-31;

Matches 194; Conservative 0; Mismatches 65; Indels 4; Gaps 3;

QY 88 ATGGGCTGCNACTATGGGCTCACCCTTCACCCANANGNGAGTACNGACGCTACTCTGGG 147

Db 276 AAGGCTCTGTAACGAGGCTCATCTCAACCAAGTGAATACAGACATACTCTGGG 335

QY 148 ACAGACCTTTTGTGNGAGATNTGCATGGCTGANGGCTTNAACCTGACTCTCGATACCAT 207

Db 336 ACAGAAATCTCTGGGAGATAAG-TTGGCTGAAGGCTTGAACCTGACGCTTGATACCAT 394

QY 208 ATTTNTACCATNCNCTCCNATCCTTTAGTGCATTTTCCCGGCTCTATTTGCCNGNAT 267

Db 395 ATTTGTACCAACACACAGGGA--AGAAGAGTGGGAAATTAAGGCCCTCTATAGACGGGAT 452

QY 268 TGTNNANNTCTCGGAGTAATGTGATNTNNAATTTTCTGACCGACGACATCTATGGCT-G 326

Db 453 TGTTTTGTCTGGGAGTAAAGTGTGACATAGATTTTCTGACCGACCATCTATGGCTGG 512

QY 327 TCTGNNNTGGCCTTTGAAGTTG 349

Db 513 GCCGTGTGGCCTTTGAAGTTG 535

RESULT 7

AF268466

LOCUS AF268466 879 bp mRNA linear MAM 29-JUN-2000

DEFINITION Bos taurus voltage-dependent anion channel 3 (VDAC3) mRNA, complete

cds.

AF268466 AF268466.1 GI:8810223

VERSION

KEYWORDS

SOURCE

ORGANISM

Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

Bovidae; Bovinae; Bos.

1 (bases 1 to 879)

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

/cell_type="lens fiber"

1..879

/gene="VDAC3"

1..23

/gene="VDAC3"

/note="design based on sequence deposited in GenBank

Accession Number NM_005662"

1..852

/gene="VDAC3"

/codon_start=1

/product="voltage-dependent anion channel 3"

/protein_id="AF80103.1"

/db_xref="GI:8810224"

/translation="MCNTPTYCDLGKAAKDVFNKGYGFGMYKIDLRKSCSGVEFSTS
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KSKLCNNFALGYKAEQDLHTHVNDGTEFGSITQVNEK IETSINLAWTAGSNNT
FGIAAKYRLDCRTSLSAKVNNASLIGLGYTQSLRPGVKLTLSALVDGKNFNAGCHKVG
LGFELEA"

BASE COUNT 264 a 179 c 218 g 218 t
ORIGIN

Query Match 38.2%; Score 133.2; DB 4; Length 879;
Best Local Similarity 73.1%; Pred. No. 1.3e-30;

Matches 193; Conservative 0; Mismatches 67; Indels 4; Gaps 3;

QY 87 CATGGCTGCNACTATGGGCTCACCCTTCACCCANANGNGAGTACNGACGCTACTCTGG 146

Db 186 CAAGATCTGTAACATGAGCTGACCTTCACGAGAGTGAACACAGACATACTCTGG 245

QY 147 GACAGACCTTTTGTGNGAGATNTGCATGGCTGANGGCTTNAACCTGACTCTCGATACCA 206

Db 246 GACAGAAATCTCTGGGAGATAAG-TTGGCTGAAGGCTTGAACCTGACTCTTGATACCA 304

QY 207 TATTTNTACCATNCNCTCCNATCCTTTAGTGCATTTTCCCGGCTCTATTTGCCNGNA 266

Db 305 TATTTGTACCGACACAGGAA--AGAAGAGTGGGAAATTAAGGCCCTCATATAACGGGA 362

QY 267 TTGNTNNANNTCTCGGAGTAATGTGATNTNNAATTTTCTGACCGACGACCATCTATGGCT- 325

Db 363 TTGTTTACGCTCTGGCAGTAATGTGATATAGATTTTCTGACGACCAACCATCTATGGCTG 422

QY 326 GTCTGNNNTGGCCTTTGAAGTTG 349

Db 423 GGCTGTGTGGCCTTTGAAGTTG 446

RESULT 8

AF048829

LOCUS AF048829 825 bp mRNA linear ROD 03-APR-1999

DEFINITION Rattus norvegicus voltage dependent anion channel 1 (RVDAC3) mRNA,

partial cds.

AF048829 AF048829.1 GI:4558731

VERSION

KEYWORDS

SOURCE

ORGANISM

Norway rat.

Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

Rattus.

1 (bases 1 to 825)

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

ARI03434	ARI03434	1393 bp	DNA	linear	PAT 14-FEB-2001
LOCUS	Sequence 5 from patent US 6087477.				
DEFINITION	ARI03434				
ACCESSION	ARI03434				
VERSION	ARI03434.1	GI:12815022			
KEYWORDS	.				
SOURCE	unknown.				
ORGANISM	unknown.				
REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 1393)				
TITLE	Falb,D.A. and Gimbrone,M.A. Jr.				
JOURNAL	Compositions and methods for the treatment and diagnosis of				
FEATURES	cardiovascular disease				
source	Patent: US 6087477-A 5 11-JUL-2000;				
	location/Qualifiers				
	1. .1393				
BASE COUNT	406 a	269 c	333 g	385 t	
ORIGIN	/organism="unknown"				
Query Match	37.4%;	Score 130.6;	DB 6;	Length 1393;	
Best Local Similarity	72.6%;	Pred. No. 8.7e-30;			
Matches 191; Conservative	0;	Mismatches 68;	Indels 4;	Gaps 3;	

Web site: <http://www.nisc.nih.gov/>
Contact: nisc_mgc@nhgri.nih.gov
Shevchenko, Y., Wetherby, K.D., Beckstrom-Sternberg, S.M.,
Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S.,
Dietrich, N.L., Guan, X., Gupta, J., Ho, S.-L., Karlins, E., Legaspi, R.,
Lim, M., Maduro, Q.L., Mastello, C., Mastrian, S.D., McCloskey, J.C.,
McDowell, J., Pearson, R., Snyder, B., Stantipop, S., Thomas, P.J.,
Tiongson, E.E., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A.,
Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/BLNI at: <http://image.llnl.gov>
Series: IRAL, Plate: 5 Row: h Column: 7
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 33293393.

FEATURES	Location/Qualifiers
source	1. .1851

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/organism="Homo sapiens"
/db_xref="LocusID:7419"
/db_xref="taxon:9606"
/clone="MGC:1966 IMAGE:3343379"
/tissue_type="Eye, retinoblastoma"
/clone_lib="NH_MGC_16"
/lab_host="DH10B-R"
/note="Vector: pOTR7"
81. .935

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/product="voltage-dependent anion channel 3"
/protein_id="AAH02456.1"
/db_xref="GI:12803281"
/translation="MCNTPTYCDLGAARDVFNKGYGFGMVKIDLKTRKSCSGVMEFST
SGHAYTDTGKASGNLETKYKVCNNGLTFTQKWNIDNTLTGEI SWENKTLAEGIKLTIIDT
IEVPNTGKKSGKLKASYKRDCEVSGSNVDIDESPTIYGWAVLAIEGVLGYOMSEFDT
AKSKLSÖNNFALGYKAADFÖLTHVNDGTIEGGSIYÖKVNKEIETSIINLAWTAGSNNT
RFGIAAKYMLDCRTSLSAKVNNASLIGLTYQTLPBGVKLTLSALIDGNFSAGGHKV
GLGFELFA"

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BASE COUNT	541 a	388 c	435 g	487 t
ORIGIN				
Query Match	37.4%	Score 130.6;	DB 9;	Length 1851;
Best Local Similarity	72.6%;	Pred. No. 8.7e-30;		
Matches 191; Conservative	0;	Mismatches 68;	Indels 4;	Gaps 3;

